

SEQUENCE LISTING

	<110>	Guo	, Gua , Ron ng, R	gbin	3												
	<120>	Rec	ombin	ant	Supe	r-Cor	npoui	nd II	nteri	fero	n						
	<130>	792	-A-PC	T-US													
	<140>	•	650,3 3-08-														
	<150> <151>		/CN02 2-02-		28												
	<150> <151>		01104 1-02-		9												
	<160>	. 13															
	<170>	Pat	entIn	ver	sion	3.2											
•	<210><211><211><212><213>	504 DNA	an sy	nthe	sis											-	
	<220><221><222>	CDS	(50	4)		•											
	<400>	. 1 :gc ga	a ata	aaa	ana	200	a aa	+ = =	a+~	~~+	224	~~+		~~+			4.0
	Met C	ys As) Leu	Pro 5	Gln	Thr	His	Ser	Leu 10	Gly	Asn	Arg	Arg	Ala 15	Leu		48
	atc c Ile L	tg cte	g gct ı Ala 20	cag Gln	atg Met	cgt Arg	cgt Arg	atc Ile 25	tcc Ser	ccg Pro	ttc Phe	tcc Ser	tgc Cys 30	ctg Leu	aaa Lys		96
	gac c Asp A	gt cad arg Hi: 35	c gac s Asp	ttc Phe	ggt Gly	ttc Phe	ccg Pro 40	cag Gln	gaa Glu	gaa Glu	ttc Phe	gac Asp 45	ggt Gly	aac Asn	cag Gln		144
	Phe G	ag aa In Ly: 0	a gct s Ala	cag Gln	gct Ala	atc Ile 55	tcc Ser	gtt Val	ctg Leu	cac His	gaa Glu 60	atg Met	atc Ile	cag Gln	cag Gln		192
	acc t Thr P 65	tc aache Asi	c ctg n Leu	ttc Phe	tcc Ser 70	acc Thr	aaa Lys	gac Asp	tcc Ser	tcc Ser 75	gct Ala	gct Ala	tgg Trp	gac Asp	gaa Glu 80		240
	tcc c Ser L	tg cto	g gaa ı Glu	aaa Lys 85	ttc Phe	tac Tyr	acc Thr	gaa Glu	ctg Leu 90	tac Tyr	cag Gln	cag Gln	ctg Leu	aac Asn 95	gac Asp		288

Leu Glu	gct Ala														336
atg aac Met Asn															384
acc ctg Thr Leu 130	Tyr														432
gtt cgt Val Arg 145															480
gaa cgt Glu Arg						taa									504
<210><211><212><213>	2 167 PRT humaı	n syr	nthes	sis								,			
<400>	2														
Met Cys 1	Asp	Leu	Pro 5	Gln	Thr	His	Ser	Leu 10	Gly	Asn	Arg	Arg	Ala 15	Leu	
			5					10	_				15		
1	Leu	Ala 20	5 Gln	Met	Arg	Arg	Ile 25	10 Ser	Pro	Phe	Ser	Cys 30	15 Leu	Lys	
1 Ile Leu	Leu His 35	Ala 20 Asp	5 Gln Phe	Met Gly Ala	Arg Phe	Arg Pro 40	Ile 25 Gln	10 Ser Glu	Pro Glu	Phe Phe	Ser Asp 45	Cys 30	15 Leu Asn	Lys Gln	
Ile Leu Asp Arg	Leu His 35 Lys	Ala 20 Asp	5 Gln Phe Gln	Met Gly Ala	Arg Phe Ile 55	Arg Pro 40 Ser	Ile 25 Gln Val	10 Ser Glu Leu	Pro Glu His	Phe Phe Glu 60	Ser Asp 45	Cys 30 Gly	15 Leu Asn Gln	Lys Gln Gln	
Ile Leu Asp Arg Phe Gln 50 Thr Phe	Leu His 35 Lys Asn	Ala 20 Asp Ala Leu	5 Gln Phe Gln	Met Gly Ala Ser 70	Arg Phe Ile 55	Arg Pro 40 Ser	Ile 25 Gln Val	10 Ser Glu Leu Ser	Pro Glu His Ser 75	Phe Phe Glu 60	Ser Asp 45 Met	Cys 30 Gly Ile	Leu Asn Gln Asp	Lys Gln Gln Glu 80	

Met A	Asn Val Asp 115	Ser Ile	Leu Ala 120	-	Lys Ty	r Phe Gln 125	Arg Ile	
	Leu Tyr Leu 130	Thr Glu	Lys Lys 135	Tyr Ser	Pro Cy	_	Glu Val	
Val <i>I</i> 145	Arg Ala Glu	Ile Met 150		Phe Ser	Leu Se	r Thr Asn	Leu Gln 160	
Glu A	Arg Leu Arg	Arg Lys 165	Glu					
<210 : <211 : <212 : <213 : <	> 360 > DNA	nthesis						
<220 > <221 > <222 >	> CDS	0)						
	> 3 tgt gat tta Cys Asp Leu							48
	ctg ctg gca Leu Leu Ala 20							96
gac o Asp A	cgt cac gac Arg His Asp 35	ttc ggc Phe Gly	ttt ccg Phe Pro 40	caa gaa Gln Glu	gag tte Glu Phe	c gat ggc e Asp Gly 45	aac caa Asn Gln	144
Phe G	cag aaa gct Gln Lys Ala 50	cag gca Gln Ala	atc tct Ile Ser 55	gta ctg Val Leu	cac gaa His Gli 60	a atg atc u Met Ile	caa cag Gln Gln	192
acc t Thr F 65	ttc aac ctg Phe Asn Leu	ttt tcc Phe Ser 70	act aaa Thr Lys	gac ago Asp Ser	tct gc Ser Ala 75	t gct tgg a Ala Trp	gac gaa Asp Glu 80	240
agc t Ser I	ttg ctg gag Leu Leu Glu	aag ttc Lys Phe 85	tac act Tyr Thr	gaa ctg Glu Leu 90	tat caq Tyr Gli	g cag ctg n Gln Leu	aac gac Asn Asp 95	288
ctg g Leu G	gaa gca tgc Glu Ala Cys 100	gta atc Val Ile	cag gaa Gln Glu	gtt ggt Val Gly 105	gta gaa Val Gli	a gag act u Glu Thr 110	ccg ctg Pro Leu	336
	aac gtc gac Asn Val Asp							360

115 120

<210> 4 <211> 120 <212> PRT

<213> human synthesis

<400> 4

Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu 1 5 10 15

Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln 35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln 50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu 65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp 85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu 100 105 110

Met Asn Val Asp Ser Ile Leu Ala 115 120

<210> 5

<211> 108

<212> DNA

<213> chemical synthesis

<220>

<221> CDS

<222> (1)..(108)

<400> 5

atg tgc gac ctg ccg cag acc cac tcc ctg ggt aac cgt cgt gct ctg Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu 1 5 10 15

48

```
atc ctg ctg gct cag atg cgt cgt atc tcc ccg ttc tcc tgc ctg aaa
                                                                       96
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
            20
                                25
gac cgt cac gac
                                                                      108
Asp Arg His Asp
        35
<210>
       6
<211>
<212>
       PRT
<213> chemical synthesis
<400> 6
Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu
                5
                                    10
Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
            20
                                25
                                                    30
Asp Arg His Asp
        35
<210> 7
<211> 107
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(107)
ctgaaagacc gtcacgactt cggtttcccg caggagaggt tcgacggtaa ccagttccag
aagctcaggc tatctccgtt ctgcacgaaa tgatccagca gaccttc
                                                                      107
<210>
       8
<211> 103
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(103)
gctgctggta cagttcggtg tagaattttt ccagcaggga ttcgtcccaa gcagcggagg
                                                                       60
```

```
agtctttggt ggagaacagg ttgaaggtct gctggatcat ttc
                                                                    103
<210> 9
<211>
      103
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(103)
<400> 9
atccctgctg gaaaaattct acaccgaact gtaccagcag ctgaacgacc tggaagcttg
                                                                     60
cgttatccag gaagttggtg ttgaagaaac cccgctgatg aac
                                                                    103
<210> 10
<211> 106
<212> DNA
<213> chemical synthesis
<220>
<221> Unsure
<222> (1)..(106)
<400> 10
gaagaaaccc cgctgatgaa cgttgactcc atcctggctg ttaaaaaata cttccagcgt
                                                                     60
atcaccctgt acctgaccga aaaaaaatac tccccgtgcg cttggg
                                                                    106
<210> 11
<211> 112
<212> DNA
<213> chemical systhesis
<220>
<221> Unsure
<222> (1)..(112)
<400> 11
ttattcttta cgacgcagac gttcctgcag gttggtggac agggagaagg aacgcatgat
                                                                     60
ttcagcacga acaacttccc aagcgcacgg ggagtatttt ttttcggtca gg
                                                                    112
<210> 12
<211> 31
<212> DNA
```

<213> chemical synthesis